

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 6, 2004, 19:35:16 ; Search time 12.1875 seconds
(without alignments)
39.474 Million cell updates/sec

Title: US-10-618-644-5

Perfect score: 27

Sequence: 1 TPRVF 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	100.0	48	2 T06450	legumin J - garden
2	27	100.0	114	2 D71177	hypothetical prote
3	27	100.0	136	2 T12140	legumin - fava bea
4	27	100.0	197	2 E69415	conserved hypothet
5	27	100.0	201	2 T46670	probable 3,5-epime
6	27	100.0	205	2 T30591	conserved hypothet
7	27	100.0	208	2 E84316	hypothetical prote
8	27	100.0	212	2 JA0152	glycinin chain A7
9	27	100.0	290	2 JC2097	legumin type B alp
10	27	100.0	329	2 S07577	legumin storage pr
11	27	100.0	335	2 S07578	legumin storage pr
12	27	100.0	335	2 S07576	legumin storage pr
13	27	100.0	335	2 D83232	hypothetical prote
14	27	100.0	335	2 T32209	hypothetical prote
15	27	100.0	350	2 S00337	legumin B Legk pre
16	27	100.0	401	2 G84160	glucose-1-phosphat
17	27	100.0	415	2 H64704	serine-tRNA ligase
18	27	100.0	446	2 E75075	hybrid cluster [4P
19	27	100.0	451	2 T23431	hypothetical prote
20	27	100.0	459	2 T40063	GPI-anchored prote
21	27	100.0	484	2 A24942	legumin B4 precurs
22	27	100.0	485	2 S44268	legumin B precurs
23	27	100.0	488	2 G81295	cytochrome-c oxida
24	27	100.0	500	2 S26688	legumin K - garden
25	27	100.0	503	2 S00336	legumin B LegJ pre
26	27	100.0	518	2 D84087	epidermal surface
27	27	100.0	521	2 T04791	hypothetical prote
28	27	100.0	545	2 S28117	gas-vesicle operon
29	27	100.0	560	2 S11004	glycinin G4 precur

glycinin chain ASA
glycinin G4 precu
glycinin ASA4B3 ch
probable legumin B
hypothetical prote
MG414 homolog Cl2-
nitrite reductase
kinesin-like prote
protein vit-6 [imp
vitellogenin vit-6
probable kinesin -
pyrimidine synthe
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote

ALIGNMENTS

RESULT 1

T06450

legumin J - garden pea (fragment)

C;Species: Pisum sativum (garden pea)

C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C;Accession: T06450

R;Brown, J.W.S.; Felix, G.; Friendewey, D.

EMBL J. 5, 2749-2758, 1986

A;Title: Accurate in vitro splicing of two pre-mRNA plant introns in a HeLa cell nuclea

A;Reference number: Z15685; MUID:87080257; PMID:2431897

A;Accession: T06450

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-48 <ERO>

A;Cross-references: UNIPROT:Q41032; EMBL:M26771; NID:g169108; PIDN:AAA33674.1; PID:g169

C;Genetics:

A;Gene: J

A;Note: intron positions not resolved (incomplete sequence)

C;Superfamily: glycinin

Query Match 100.0%; Score 27; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TPRVF 5

Db 14 TPRVF 18

RESULT 2

D71177

hypothetical protein PH1698 - Pyrococcus horikoshii

C;Species: Pyrococcus horikoshii

C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004

C;Accession: D71177

R;Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Seki

M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguch

DNA Res. 5, 55-76, 1998

A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic

A;Reference number: A71000; MUID:98344137; PMID:9679194

A;Accession: D71177

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-114 <KAW>

A;Cross-references: UNIPROT:O59363; GB:AP000007; NID:g3236134; PIDN:BA30811.1; PID:g32

A;Experimental source: strain OT3

A;Note: this accession replaces an interim accession for a sequence replaced by GenBank

C;Genetics:

A;Gene: PH1698

Query Match 100.0%; Score 27; DB 2; Length 114;

Best Local Similarity 100.0%; Pred. No. 25;

```

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPRVF 5
    |||||
Db 104 TPRVF 108

RESULT 3
T12140
legumin - fava bean (fragment)
C:Species: Vicia faba (fava bean)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T12140
R:Heim, U.; Baeumlein, H.; Wobus, U.
Plant Mol. Biol. 25, 131-135, 1994
A>Title: The legumin gene family: a reconstructed Vicia faba legumin gene encoding a high molecular weight protein
A:Reference number: S46503; MUID:94272010; PMID:8003694
A:Accession: T12140
A:Molecule type: DNA
A:Residues: 1-136 <HEI>
A:Cross-references: UNIPROT:Q43672; EMBL:Z26487; NID:9403333; PIDN:CAA81261.1; PID:9403333
C:Genetics:
A:Gene: Le1B161
A:Note: Intron positions not resolved (incomplete sequence)
C:Superfamily: glycinin
C:Keywords: seed; storage protein

Query Match 100.0%; Score 27; DB 2; Length 136;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPRVF 5
    |||||
Db 84 TPRVF 88

RESULT 4
E69415
conserved hypothetical protein AF1326 - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: E69415
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, J.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.; Smith, H.O.; Woese, C.R.; Venter, J.C.
A>Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeon Pyrococcus furiosus
A:Reference number: A69250; MUID:98049343; PMID:9389475
A:Accession: E69415
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-197 <KLE>
A:Cross-references: UNIPROT:O28943; GB:AE001012; GB:AE000782; NID:92689335; PIDN:AAB8991
C:Superfamily: hypothetical protein MJ0320; translation elongation factor Tu homology
C:Keywords: GTP binding; nucleotide binding; P-loop
F;10-17/Region: nucleotide-binding motif A (P-loop)
F;132-135/Region: GTP-binding NKXD motif
F;174-176/Region: GTP-binding SAK/L motif

Query Match 100.0%; Score 27; DB 2; Length 197;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPRVF 5
    |||||
Db 124 TPRVF 128

RESULT 5
T46670
probable 3,5-epimerase nogF [imported] - Streptomyces nogalater
C:Species: Streptomyces nogalater
C>Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 09-Jul-2004
C:Accession: T46670
R:Ylihanko, K.P.J.
Submitted to the EMBL Data Library, October 1999
A:Reference number: Z23126
A:Accession: T46670
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-201 <YLI>
A:Cross-references: UNIPROT:O54257; EMBL:AJ224512; PIDN:CAA12011.1
A:Experimental source: ATCC 27451
C:Genetics:
A:Gene: snogF
C:Superfamily: dTDP-4-dehydrorhamnose 3,5-epimerase

Query Match 100.0%; Score 27; DB 2; Length 201;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPRVF 5
    |||||
Db 15 TPRVF 19

RESULT 6
T30591
conserved hypothetical protein PCZA361.16 - Amycolatopsis orientalis
C:Species: Amycolatopsis orientalis
C>Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C:Accession: T30591
R:Van Wageningen, A.; Kirkpatrick, P.; Williams, D.; Harris, B.; Kershaw, J.; Lennard, N.
Chem. Biol. 3, 155-162, 1998
A>Title: Sequencing and analysis of genes involved in the biosynthesis of a vancomycin G
A:Reference number: Z18804
A:Accession: T30591
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-205 <VAN>
A:Cross-references: UNIPROT:O52806; EMBL:AJ223998
C:Superfamily: dTDP-4-dehydrorhamnose 3,5-epimerase

Query Match 100.0%; Score 27; DB 2; Length 205;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPRVF 5
    |||||
Db 15 TPRVF 19

RESULT 7
E84316
hypothetical protein Vng1641h [imported] - Halobacterium sp. NRC-1
C:Species: Halobacterium sp. NRC-1
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: E84316
R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithausen, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabcic, J.; Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li, A.; Title: Genome sequence of Halobacterium species NRC-1
A:Reference number: A84160; MUID:20504483; PMID:11016950
A:Accession: E84316
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-208 <STO>
A:Cross-references: UNIPROT:Q9HPHO; GB:AE004437; NID:910581111; PIDN:AAG19897.1; GSPDB:C
C:Genetics:
A:Gene: VNG1641H

```

Query Match 100.0%; Score 27; DB 2; Length 208;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPRVF 5
Db 145 TPRVF 149

RESULT 8
JA0152
glycinin chain A7 - soybean
N:Alternate names: seed storage protein
C:Species: Glycine max (soybean)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 24-Feb-1995
C:Accession: JA0152
R:Kagawa, H.; Hirano, H.
Plant Sci. 56, 189-195, 1988
A:Title: Identification and structural characterization of the glycinin seed storage protein
A:Reference number: JA0152
A:Accession: JA0152
A:Molecule type: protein
A:Residues: 1-212 <KAG>
A:Experimental source: seed
C:Comment: Glycinin is the most abundant protein in the soybean seeds. A7 chain is one of the most abundant protein in the soybean seeds. A7 chain is one of the most abundant protein in the soybean seeds.
C:Superfamily: glycinin

Query Match 100.0%; Score 27; DB 2; Length 212;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPRVF 5
Db 63 TPRVF 67

RESULT 9
JC2097
legumin type B alpha chain precursor (clone LeB4, B4) - tick bean
C:Species: Vicia faba var. minor (tick bean)
C:Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 06-Dec-1996
C:Accession: JC2097
R:Horstmann, C.; Schlesier, B.; Otto, A.; Kostka, S.; Muentz, K.
Theor. Appl. Genet. 86, 867-874, 1993
A:Title: Polymorphism of legumin subunits from field bean (Vicia faba L. var. minor) and from tick bean (Vicia faba var. minor)
A:Reference number: JC2094
A:Accession: JC2097
A:Molecule type: DNA
A:Residues: 1-290 <HOR>
C:Superfamily: glycinin

Query Match 100.0%; Score 27; DB 2; Length 290;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPRVF 5
Db 181 TPRVF 185

RESULT 10
S07577
legumin storage protein LeB6 - fava bean (fragment)
C:Species: Vicia faba (fava bean)
C:Date: 21-Nov-1993 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C:Accession: S07577
R:Heim, U.; Schubert, R.; Baumelein, H.; Wobus, U.
Plant Mol. Biol. 13, 653-663, 1989
A:Title: The legumin gene family: structure and evolutionary implications of Vicia faba
A:Reference number: S07576; MUID:91370849; PMID:2491681

A:Accession: S07577
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-329 <HEI>
A:Cross-references: UNIPROT:P16079; EMBL:X14240; NID:g22020; PIDN:CAA32456.1; PID:g29584

C:Genetics:
A:Gene: LeB6
A:Introns: 34/3; 204/3
C:Superfamily: glycinin
C:Keywords: seed; storage protein

Query Match 100.0%; Score 27; DB 2; Length 329;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPRVF 5
Db 32 TPRVF 36

RESULT 11
S07578
legumin storage protein LeB7 - fava bean (fragment)
C:Species: Vicia faba (fava bean)
C:Date: 21-Nov-1993 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C:Accession: S07578
R:Heim, U.; Schubert, R.; Baumelein, H.; Wobus, U.
Plant Mol. Biol. 13, 653-663, 1989
A:Title: The legumin gene family: structure and evolutionary implications of Vicia faba
A:Reference number: S07576; MUID:91370849; PMID:2491681
A:Accession: S07578
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-335 <HEI>
A:Cross-references: UNIPROT:P16080; EMBL:X14241; NID:g22024; PIDN:CAA32457.1; PID:g2958

C:Genetics:
A:Gene: LeB7
A:Introns: 34/3; 210/3
C:Superfamily: glycinin
C:Keywords: seed; storage protein

Query Match 100.0%; Score 27; DB 2; Length 335;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPRVF 5
Db 32 TPRVF 36

RESULT 12
S07576
legumin storage protein LeB2 - fava bean (fragment)
C:Species: Vicia faba (fava bean)
C:Date: 21-Nov-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C:Accession: S07576
R:Heim, U.; Schubert, R.; Baumelein, H.; Wobus, U.
Plant Mol. Biol. 13, 653-663, 1989
A:Title: The legumin gene family: structure and evolutionary implications of Vicia faba
A:Reference number: S07576; MUID:91370849; PMID:2491681
A:Accession: S07576
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-335 <HEI>
A:Cross-references: UNIPROT:P16078; EMBL:X14237; NID:g22013; PIDN:CAA32454.1; PID:g2958

C:Genetics:
A:Gene: LeB2
A:Introns: 34/3; 210/3
C:Superfamily: glycinin
C:Keywords: seed; storage protein

Query Match 100.0%; Score 27; DB 2; Length 335;
Best Local Similarity 100.0%; Pred. No. 72;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPRVF 5
|||||
Db 32 TPRVF 36

RESULT 13

D83232
hypothetical protein PA3313 [imported] - Pseudomonas aeruginosa (strain PA01)
C/Species: Pseudomonas aeruginosa
C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C/Accession: D83232
R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Boman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
A/Reference number: A82950; MUID:20437337; PMID:10984043
A/Accession: D83232
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-335 <STO>
A/Cross-references: UNIPROT:Q9HYT1; GB:AE004753; GB:AE004091; NID:g9949433; PIDN:AAG0670
A/Experimental source: strain PA01
C/Genetics:
A/Gene: PA3313

Query Match 100.0%; Score 27; DB 2; Length 335;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPRVF 5
|||||
Db 37 TPRVF 41

RESULT 14

T32209
hypothetical protein T03D3.2 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C/Accession: T32209
R/Murray, J.; Wohldmann, P.; Bauer, C.; Biewald, T.
submitted to the EMBL Data Library, September 1997
A/Description: The sequence of C. elegans cosmid T03D3.
A/Reference number: Z21136
A/Accession: T32209
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: DNA
A/Residues: 1-335 <MUR>
A/Cross-references: UNIPROT:O16981; EMBL:AF022980; PIDN:AAB69919.1; GSPDB:GN00023; CBSP:
A/Experimental source: strain Bristol N2, clone T03D3
C/Genetics:
A/Gene: CBSP:T03D3.2
A/Map position: 5
A/Introns: 63/3; 186/3; 220/3; 277/2

Query Match 100.0%; Score 27; DB 2; Length 335;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPRVF 5
|||||
Db 10 TPRVF 14

RESULT 15

S00337
legumin B LegK precursor - garden pea (fragment)
N/Alternate names: minor legumin legk
C/Species: Pisum sativum (garden pea)
C/Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004

C/Accession: S00337; S02306
R/Gatehouse, J.A.; Bown, D.; Gilroy, J.; Levasseur, M.; Castleton, J.; Ellis, T.H.N.
Biochem. J. 250, 15-24, 1988
A/Title: Two genes encoding 'minor' legumin polypeptides in pea (Pisum sativum L.). Characterization of the amino acid sequences of the beta chain, was confirmed
A/Reference number: S00336; MUID:88183306; PMID:3355508
A/Accession: S00337
A/Molecule type: DNA
A/Residues: 1-350 <GAT>
A/Cross-references: UNIPROT:P05693; EMBL:X07015; NID:g20784; PIDN:CAA30068.1; PID:g20785
A/Note: part of this sequence, including the amino end of the beta chain, was confirmed
R/Domoney, C.; Barker, D.; Casey, R.
Plant Mol. Biol. 7, 467-474, 1986
A/Title: The complete deduced amino acid sequences of legumin beta-polypeptides from different Pisum sativum L. accessions
A/Reference number: S02306
A/Accession: S02306
A/Molecule type: mRNA
A/Residues: 132-350 <DOM>
A/Cross-references: EMBL:M16903
A/Note: the nucleotide sequence contains a frameshift in codon 131
A/Reference number: S02306
A/Note: translation of nucleotide sequence for residues 132-169 is not given
C/Genetics:
A/Gene: LegK
A/Map position: 1
A/Introns: 33/3, 225/3
C/Superfamily: Glycinin
F:170-350/Product: legumin B alpha chain (fragment) #status experimental <ACH>
F:170-350/Product: legumin B beta chain #status experimental <BCH>

Query Match 100.0%; Score 27; DB 2; Length 350;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPRVF 5
|||||
Db 31 TPRVF 35

Search completed: November 6, 2004, 19:54:16
Job time : 13.1875 secs